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ARAND et al
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SEQUENCE LISTING

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FURSTOSS, ROLAND

<120> EPOXIDE HYDROLASES OF ASPERGILLUS ORIGIN

<130> bml-410.018

<140> 10/009,030
<141> 2001-11-02

<150> PCT/FR00/01217
<151> 2000-05-05

<150> FR 99/05711
<151> 1999-05-05

<160> 8

<170> PatentIn Ver. 2.1

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<212> DNA
<213> *Aspergillus niger*

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<221> CDS
<222> (1) . . (1194)

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Met Ser Ala Pro Phe Ala Lys Phe Pro Ser Ser Ala Ser Ile Ser Pro
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aat cct ttc acg gtc tct atc ccg gat gaa cag ttg gat gac ttg aaa 96
Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
          20           25           30

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acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
35 40 45

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caa gcg gat ggc cg50 ttt ggc atc act tct gaa tgg ctg aca act atg 192
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
      55           60

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ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
85          90          95

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cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca	336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala	
100 105 110	
ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg	384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu	
115 120 125	
cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg	432
Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu	
130 135 140	
gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg	480
Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu	
145 150 155 160	
gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg	528
Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu	
165 170 175	
atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat	576
Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp	
180 185 190	
att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc	624
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys	
195 200 205	
aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc	672
Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly	
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ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga	720
Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg	
225 230 235 240	
atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt	768
Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser	
245 250 255	
act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca	816
Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala	
260 265 270	
tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc	864
Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro	
275 280 285	
ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg	912
Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr	
290 295 300	
gaa agt ttc ccg cgg gca att cat acc tac cgc gag act acc cca act	960
Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr	
305 310 315 320	

gcc tcc gct ccc aat gga gcg aca atg ctt cag aag gaa tta tat att 1008
Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
325 330 335

cac aag ccg ttt ggg ttc tcc ttc ccc aag gac ctt tgt cct gtg 1056
His Lys Pro Phe Gly Phe Ser Phe Pro Lys Asp Leu Cys Pro Val
340 345 350

cct cgg agc tgg att gct aca acg gga aat cta gta ttc ttc cgg gat 1104
Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
355 360 365

cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152
His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
370 375 380

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<211> 398

<212> PRT

<213> Aspergillus niger

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Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
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Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
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Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
85 90 95

His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
115 120 125

Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
130 135 140

Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu
145 150 155 160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
165 170 175
Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp
180 185 190
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys
195 200 205
Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
210 215 220
Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
225 230 235 240
Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
245 250 255
Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Ser Pro Ile Ala
260 265 270
Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
275 280 285
Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
290 295 300
Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
305 310 315 320
Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
325 330 335
His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val
340 345 350
Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
355 360 365
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Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
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<223> Description of Artificial Sequence: Primer

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<212> DNA
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<210> 6
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 6
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<210> 7
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<212> DNA
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<223> Description of Artificial Sequence: Primer

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<213> Artificial Sequence

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44

SEQUENCE LISTING

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5 <120> PROTEINS OF FUNGAL ORIGIN AND DERIVATIVES,
PROCESSES FOR OBTAINING THEM, AND THEIR USES, IN
PARTICULAR FOR THE PREPARATION OF ENANTIOMERICALLY
PURE MOLECULES

10 <130> EPOXSL

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15 <160> 2

<170> PatentIn Ver. 2.1

<210> 1

20 <211> 1197

<212> DNA

<213> Aspergillus niger

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Nucleotide sequence SEQ ID NO : 1

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Asn Pro Phe Thr Val Ser Ile Pro Asp Glu Gln Leu Asp Asp Leu Lys
20 25 3040 acc ctc gtc cga ctg tcc aag att gct cct ccc acc tat gag agc ctg 144
Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
35 40 4545 caa gcg gat ggc cgg ttt ggc atc act tct gaa tgg ctg aca act atg 192
Gln Ala Asp Gly Arg Phe Gly Ile Thr Ser Glu Trp Leu Thr Thr Met
50 55 6050 cgg gag aaa tgg ctc tcg gag ttt gac tgg cga cca ttt gaa gct cga 240
Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
65 70 75 8055 ctg aac tct ttc cct cag ttt act aca gag atc gag ggt ctc acg att 288
Leu Asn Ser Phe Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
85 90 9560 cac ttt gct gct ctc ttc tcc gag agg gag gat gct gtg cct atc gca 336
His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
100 105 11065 ttg ctc cat ggt tgg ccc ggc agc ttc gtt gag ttc tac cca atc ctg 384
Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
115 120 125

5	cag cta ttc cgg gag gag tac acc cct gag act ctg cca ttc cat ctg Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu 130 135 140	432
10	gtt gtt ccg tcc ctt cct ggg tat act ttt tca tct ggt ccc ccg ctg Val Val Pro Ser Leu Pro Gly Tyr Thr Phe Ser Ser Gly Pro Pro Leu 145 150 155 160	480
15	gac aag gac ttc ggc ttg atg gac aac gcc cgg gtc gta gac cag ttg Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu 165 170 175	528
20	atg aag gac ctc ggg ttc gga agt ggt tat att att cag gga ggt gat Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Gly Asp 180 185 190	576
25	att ggt agc ttt gtt gga cga ctg ttg ggc gtg ggt ttc gac gcc tgc Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys 195 200 205	624
30	aaa gcg gtt cat ttg aac ctg tgc gca atg agg gct ccc cct gag ggc Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly 210 215 220	672
35	ccg tca att gag agc ttg tcc gca gcg gag aag gag gga atc gcg cga Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg 225 230 235 240	720
40	atg gag aag ttc atg acc gat ggc tta gct tat gcc atg gag cac agt Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser 245 250 255	768
45	act cgg ccc agt act att ggc cac gtg ctg tcc agc agt ccg atc gca Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala 260 265 270	816
50	tta ctt gca tgg att ggt gag aaa tat ctc caa tgg gtg gat aaa ccc Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro 275 280 285	864
55	ctc cct tct gag acc atc ctc gag atg gtg agc ctg tat tgg ctg acg Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr 290 295 300	912
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	cac aag ccg ttt ggg ttc tcc ttc ccc aag gac ctt tgt cct gtg His Lys Pro Phe Gly Phe Ser Phe Phe Pro Lys Asp Leu Cys Pro Val 340 345 350	1056
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cat gca gag gga gga cac ttt gcc gca ttg gag cgt cca cgc gag ctg 1152
His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
.370 375 380

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5 aag acc gac ctg aca gca ttt gtc gag cag gtg tgg cag aag tag 1197
 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
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<213> Aspergillus niger

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Thr Leu Val Arg Leu Ser Lys Ile Ala Pro Pro Thr Tyr Glu Ser Leu
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50 55 60

30 Arg Glu Lys Trp Leu Ser Glu Phe Asp Trp Arg Pro Phe Glu Ala Arg
 65 70 75 80

Leu Asn Ser Phe Pro Gln Phe Thr Thr Glu Ile Glu Gly Leu Thr Ile
85 90 95

35 His Phe Ala Ala Leu Phe Ser Glu Arg Glu Asp Ala Val Pro Ile Ala
100 105 110

Leu Leu His Gly Trp Pro Gly Ser Phe Val Glu Phe Tyr Pro Ile Leu
 115 120 125

40 Gln Leu Phe Arg Glu Glu Tyr Thr Pro Glu Thr Leu Pro Phe His Leu
 130 135 140

Val	Val	Pro	Ser	Leu	Pro	Gly	Tyr	Thr	Phe	Ser	Ser	Gly	Pro	Pro	Leu
145					150					155					160

Asp Lys Asp Phe Gly Leu Met Asp Asn Ala Arg Val Val Asp Gln Leu
 165 170 175

50 Met Lys Asp Leu Gly Phe Gly Ser Gly Tyr Ile Ile Gln Gly Glu Asp

180 185 190
Ile Gly Ser Phe Val Gly Arg Leu Leu Gly Val Gly Phe Asp Ala Cys

55 195 200 205
 Lys Ala Val His Leu Asn Leu Cys Ala Met Arg Ala Pro Pro Glu Gly
 210 215 220

60 Pro Ser Ile Glu Ser Leu Ser Ala Ala Glu Lys Glu Gly Ile Ala Arg
 225 230 235 240

Met Glu Lys Phe Met Thr Asp Gly Leu Ala Tyr Ala Met Glu His Ser
245 250 255

5 Thr Arg Pro Ser Thr Ile Gly His Val Leu Ser Ser Pro Ile Ala
260 265 270

Leu Leu Ala Trp Ile Gly Glu Lys Tyr Leu Gln Trp Val Asp Lys Pro
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Leu Pro Ser Glu Thr Ile Leu Glu Met Val Ser Leu Tyr Trp Leu Thr
290 295 300

15 Glu Ser Phe Pro Arg Ala Ile His Thr Tyr Arg Glu Thr Thr Pro Thr
305 310 315 320

Ala Ser Ala Pro Asn Gly Ala Thr Met Leu Gln Lys Glu Leu Tyr Ile
20 325 330 335

His Lys Pro Phe Gly Phe Ser Phe Pro Lys Asp Leu Cys Pro Val
340 345 350

Pro Arg Ser Trp Ile Ala Thr Thr Gly Asn Leu Val Phe Phe Arg Asp
25 355 360 365

His Ala Glu Gly Gly His Phe Ala Ala Leu Glu Arg Pro Arg Glu Leu
370 375 380

30 Lys Thr Asp Leu Thr Ala Phe Val Glu Gln Val Trp Gln Lys
385 390 395